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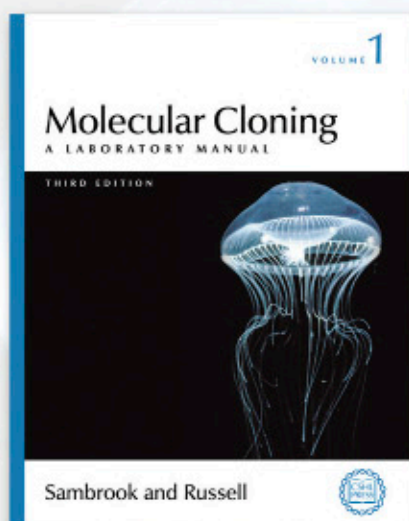
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Prepare Small-RNA Libraries with Greatly Reduced Adaptor-Dimer Background

The ScriptMiner™ Small RNA-Seq Library Preparation Kits provide an improved process for preparing second-generation sequencing libraries from the entire small-RNA transcriptome. The unique enzymatic process* dramatically reduces adaptor dimers that can cause high background in conventional small-RNA library preparations.

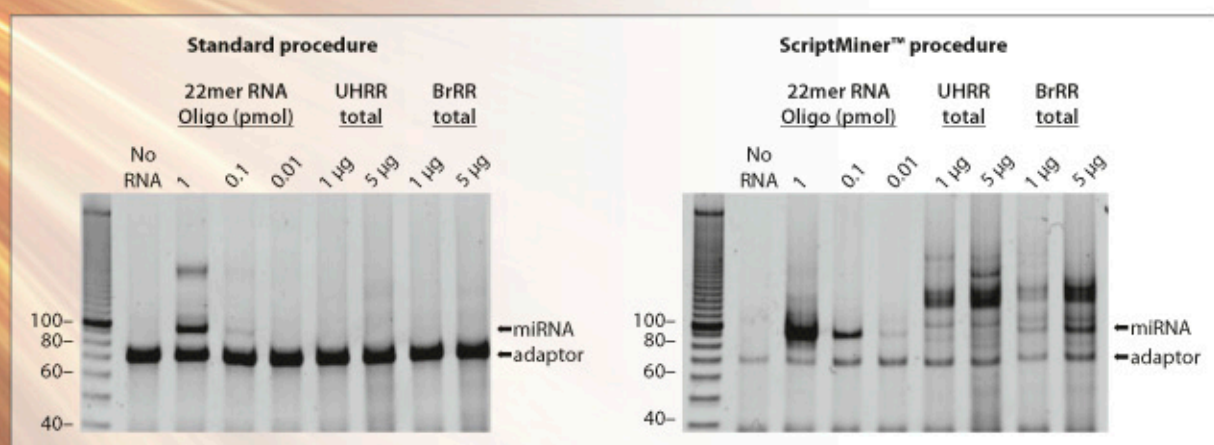
- Produce libraries in 1 day from small RNAs such as miRNA and, optionally, small capped RNA.
- Enable directional sequencing of the library.
- Start with total RNA (1-5 µg) or size-selected RNA (100 pg).
- Obtain more comprehensive capture and sequencing of small RNAs, through an optimized ligation process.

Kits for preparing singleplex (nonbarcoded) or multiplex (barcoded) libraries are available.

**Patent pending*

Summary of sequencing data from ScriptMiner™ libraries.
BrRR, Brain Reference RNA.

RNA Sample	Kit Format	Reads Passing Filter	Reads Aligned to hg19	% Aligned
BrRR	Singleplex	17,272,948	16,823,979	97.40
BrRR	Multiplex	1,384,314	1,380,799	99.75
HeLa	Multiplex	1,560,105	1,555,406	99.70



The ScriptMiner™ procedure substantially reduces adaptor-dimer background. The indicated RNA samples were used to prepare small-RNA libraries, using either a conventional procedure or the ScriptMiner procedure. Samples were examined by denaturing polyacrylamide gel electrophoresis after 12 cycles of PCR. UHRR, Universal Human Reference RNA; BrRR, Brain Reference RNA.

ScriptSeq™ mRNA Library Preparation Kits are also available. For more information, visit:
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The candidates will hold a Research Faculty position. Review of the applications will begin on December 1, 2010 and continue until the positions are filled. Please submit curriculum vitae, a description of research interests and three letters of reference to:

Shrikant Mane, Director, Yale Center for Genome Analysis
Yale University School of Medicine
Department of Genetics
PO Box 208005
New Haven, Ct., 06520-8005
Telephone: (203) 737-3058
E-mail: shrikant.mane@yale.edu

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Candidates must have the desire and ability to work collaboratively as part of a team. Ideal candidates must have a Ph.D. degree in a related field (Biology, Computer Science, Mathematics or Physical Sciences), excellent communication skills and strong programming skills. Proficiency in Python, Ruby or Perl, C or C++, as well as R is desired.

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Additional Meetings of Interest:

**Genetics, Immunology
and Repair in Multiple Sclerosis**
February 15–20, 2011
Taos, New Mexico, USA
www.keystonesymposia.org/11B8

**DNA Replication and
Recombination**
February 27–March 1, 2011
Keystone, Colorado, USA
www.keystonesymposia.org/11C2

Omics Meets Cell Biology
May 8–13, 2011
Alpbach, Austria
www.keystonesymposia.org/11E1

Genomic Instability and DNA Repair

Scientific Organizers: Junjie Chen, Karlene A. Cimprich and Michael B. Yaffe

January 30–February 4, 2011

Keystone Resort • Keystone, Colorado • USA

Keynote Speakers: David M. Livingston, Dana-Farber Cancer Institute, USA

"Genomic Instability and Breast Cancer"

Stephen J. Elledge, Harvard-Partners Center for Genetics and Genomics, USA

"The DNA Damage Response: Making it Safe to Play with Knives"

www.keystonesymposia.org/11B4

Evolutionary Developmental Biology

Scientific Organizers: Sean B. Carroll, Trisha Wittkopp and Nicole King

February 27–March 3, 2011

Granlibakken Resort • Tahoe City, California • USA

Keynote Speaker: Neil Shubin, University of Chicago, USA

"Fossils, Genes and the Evolution of the Vertebrate Limb"

www.keystonesymposia.org/11C1

Environmental Genomics and Disease Susceptibility

Scientific Organizers: Randy L. Jirtle, Moshe Szyf and Frederick L. Tyson

March 27–April 1, 2011

Grove Park Inn Resort & Spa • Asheville, North Carolina • USA

Keynote Speaker: Matt Ridley, Blagdon Seaton Burn, UK

"Nature via Nurture"

www.keystonesymposia.org/11D3

Changing Landscape of the Cancer Genome

Scientific Organizers: Lynda Chin, Christoph Lengauer and Michael Stratton

June 20–25, 2011

Boston Park Plaza Hotel & Towers • Boston, Massachusetts • USA

Keynote Speaker: Tom Hudson, Ontario Institute for Cancer Research, Canada

"Large-Scale Cancer Genomics"

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